

10088356.072202



PCT

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/088,356

DATE: 08/20/2002 P-6
 TIME: 09:08:58

Input Set : A:\EP.txt
 Output Set: N:\CRF4\08202002\J088356.raw

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3 <110> APPLICANT: TRUCKSIS, Michele
5 <120> TITLE OF INVENTION: VIRULENCE GENES OF M. MARINUM AND M. TUBERCULOSIS
7 <130> FILE REFERENCE: VET 1 WO
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/088,356
C--> 10 <141> CURRENT FILING DATE: 2002-07-22
12 <160> NUMBER OF SEQ ID NOS: 46
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 18
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
24 <400> SEQUENCE: 1
25 ctaggtacct acaacctc 18
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 18
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
36 <400> SEQUENCE: 2
37 catggtaccc attctaac 18
40 <210> SEQ ID NO: 3
41 <211> LENGTH: 89
42 <212> TYPE: DNA
43 <213> ORGANISM: Artificial Sequence
45 <220> FEATURE:
46 <223> OTHER INFORMATION: Description of Artificial Sequence: template RT1
47 oligonucleotide
49 <220> FEATURE:
50 <223> OTHER INFORMATION: "n" represents a, t, c, g, other or unknown
52 <400> SEQUENCE: 3
W--> 53 ctaggtacct acaacctcaa gcttnknknk nknknknknk nknknknknk nknknknknk 60
W--> 54 nknkaagctt ggtagaatg ggtaccatg 89
57 <210> SEQ ID NO: 4
58 <211> LENGTH: 169
59 <212> TYPE: DNA
60 <213> ORGANISM: Mycobacterium marinum
62 <220> FEATURE:
63 <223> OTHER INFORMATION: Mutant 41.2
65 <220> FEATURE:
66 <223> OTHER INFORMATION: "n" represents a, t, c, g, other or unknown

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68 <400> SEQUENCE: 4
W--> 69 cgggccgcatc tatgacgagn acgacgggac agatgggtcc ccggatggtc tacaccgaga 60
70 ccaaactgaa ctcgtcgttc tccttcggcg ggcccaagtg tctggtgaag gtgatccaaa 120
71 aactgtccgg gttgagcatc aaccgggttca tcgccatcga ctctgctcg 169
74 <210> SEQ ID NO: 5
75 <211> LENGTH: 55
76 <212> TYPE: PRT
77 <213> ORGANISM: Mycobacterium marinum
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Mutant 41.2
82 <220> FEATURE:
83 <223> OTHER INFORMATION: "Xaa" represents any, other or unknown amino acid
85 <400> SEQUENCE: 5
W--> 86 Gly Arg Ser Met Thr Xaa Thr Thr Gly Gln Met Gly Pro Arg Met Val
87 1 5 10 15
89 Tyr Thr Glu Thr Lys Leu Asn Ser Ser Phe Ser Phe Gly Gly Pro Lys
90 20 25 30
92 Cys Leu Val Lys Val Ile Gln Lys Leu Ser Gly Leu Ser Ile Asn Arg
93 35 40 45
95 Phe Ile Ala Ile Asp Phe Val
96 50 55
99 <210> SEQ ID NO: 6
100 <211> LENGTH: 382
101 <212> TYPE: DNA
102 <213> ORGANISM: Mycobacterium marinum
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Mutant 80.1
107 <220> FEATURE:
108 <223> OTHER INFORMATION: "n" represents a, t, c, g, other or unknown
110 <400> SEQUENCE: 6
W--> 111 acctcctgaa tgtgtgacat ggccctagaa ccctgcntta gactatttac atacatggct 60
112 tcacccggcc gcctgtgcca ctcataagac tactggaatg gaccaacaat cgcacagtca 120
113 tctgaagcag gagtctgtta atcacaggcc ctgaaggaa agtgactgtg cagagaaaga 180
114 cggcaatgca tcctgttaac taagtggctg gaggagtgcc aggtcattcc aaagaacatc 240
W--> 115 cctgaaatct ggaggagaag gtatagttag caccacaaa tttcaactgg agacatcana 300
116 ccagagtctc tactgagctg ccaagcttgc ggccgcactc gagtaactag ttaaccctt 360
117 ggggcctcta aacgggtctt ga 382
120 <210> SEQ ID NO: 7
121 <211> LENGTH: 121
122 <212> TYPE: PRT
123 <213> ORGANISM: Mycobacterium marinum
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Mutant 80.1
128 <220> FEATURE:
129 <223> OTHER INFORMATION: "Xaa" represents any, other or unknown amino acid
131 <400> SEQUENCE: 7
133 Pro Pro Glu Cys Val Thr Trp Pro Asn Pro Ala Leu Asp Tyr Leu His
134 1 5 10 15
136 Thr Trp Leu His Pro Ala Ala Cys Ala Thr His Lys Thr Thr Gly Met

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137          20          25          30
139 Asp Gln Gln Ser His Ser His Leu Lys Gln Glu Ser Val Asn His Arg
140          35          40          45
142 Pro Arg Asn Ser Asp Cys Ala Glu Lys Asp Gly Asn Ala Ser Cys Leu
143          50          55          60
145 Ser Gly Trp Arg Ser Ala Arg Ser Phe Gln Arg Thr Ser Leu Lys Ser
146 65          70          75          80
148 Gly Gly Glu Gly Ile Val Ser Thr Pro Lys Phe Gln Leu Glu Thr Ser
149          85          90          95
W--> 151 Xaa Gln Ser Leu Tyr Ala Ala Lys Leu Ala Ala Ala Leu Glu Leu Val
152          100          105          110
154 Asn Pro Leu Gly Pro Leu Asn Gly Ser
155          115          120
158 <210> SEQ ID NO: 8
159 <211> LENGTH: 172
160 <212> TYPE: DNA
161 <213> ORGANISM: Mycobacterium marinum
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Mutant 86.1
166 <400> SEQUENCE: 8
167 tcatcgctaa ccggttgagc taccgcccgc acagcgtgcc catcatctcc aacctgaccg 60
168 gtcacttgcc cacagtcgag caactcacat cgccccgcta ttgggcacag catgtacggg 120
169 agccagtgcg gtttcatgac ggcgttaccg gcttggtggc aggcggagaa ca 172
172 <210> SEQ ID NO: 9
173 <211> LENGTH: 55
174 <212> TYPE: PRT
175 <213> ORGANISM: Mycobacterium marinum
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Mutant 86.1
180 <400> SEQUENCE: 9
181 Ala Asn Arg Leu Ser Tyr Arg Pro His Ser Val Pro Ile Ile Ser Asn
182 1          5          10          15
184 Leu Thr Gly Ser Leu Ala Thr Val Glu Gln Leu Thr Ser Pro Arg Tyr
185          20          25          30
187 Trp Ala Gln His Val Arg Glu Pro Val Arg Phe His Asp Gly Val Thr
188          35          40          45
190 Gly Leu Leu Ala Gly Gly Glu
191          50          55
194 <210> SEQ ID NO: 10
195 <211> LENGTH: 228
196 <212> TYPE: DNA
197 <213> ORGANISM: Mycobacterium marinum
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Mutant 62.2
202 <400> SEQUENCE: 10
203 gatccggtgc cgccttgacc ggccgcgccca ccagtaccgc cgacgccgcc ctggccgccg 60
204 gcttgtgcgg cttgcgatgg gtcggtgctg tcggtgccgg tgcctccggt gccgccttgg 120
205 cctccggttc cgccggtgcc gccctggccg ccgggcctt ggatgccgcc ggtgccggtt 180
206 ccggtgcac cgccggttcc gccggttccg cctgcgccgc cggtgcct 228

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209 <210> SEQ ID NO: 11
210 <211> LENGTH: 225
211 <212> TYPE: DNA
212 <213> ORGANISM: Mycobacterium marinum
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Mutant 62.2
217 <220> FEATURE:
218 <221> NAME/KEY: CDS
219 <222> LOCATION: (1)..(225)
221 <400> SEQUENCE: 11
222 ggc acc ggc ggc gca ggc gga acc ggc gga acg ggc ggt gca gcc gga 48
223 Gly Thr Gly Gly Ala Gly Gly Thr Gly Gly Thr Gly Gly Ala Ala Gly
224 1 5 10 15
226 acc ggc acc ggc ggc atc caa ggc gcc ggc ggc cag ggc ggc acc ggc 96
227 Thr Gly Thr Gly Gly Ile Gln Gly Ala Gly Gly Gln Gly Gly Thr Gly
228 20 25 30
230 gga acc gga ggc caa ggc ggc acc gga ggc acc ggc acc gac agc acc 144
231 Gly Thr Gly Gly Gln Gly Gly Thr Gly Gly Thr Gly Thr Asp Ser Thr
232 35 40 45
234 gac cca tcg caa gcc gca caa gcc ggc ggc cag ggc ggc gtc ggc ggt 192
235 Asp Pro Ser Gln Ala Ala Gln Ala Gly Gly Gln Gly Gly Val Gly Gly
236 50 55 60
238 act ggt ggc gcg gcc ggt caa ggc ggc acc gga 225
239 Thr Gly Gly Ala Ala Gly Gln Gly Gly Thr Gly
240 65 70 75
243 <210> SEQ ID NO: 12
244 <211> LENGTH: 75
245 <212> TYPE: PRT
246 <213> ORGANISM: Mycobacterium marinum
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Mutant 62.2
251 <400> SEQUENCE: 12
252 Gly Thr Gly Gly Ala Gly Gly Thr Gly Gly Thr Gly Gly Ala Ala Gly
253 1 5 10 15
255 Thr Gly Thr Gly Gly Ile Gln Gly Ala Gly Gly Gln Gly Gly Thr Gly
256 20 25 30
258 Gly Thr Gly Gly Gln Gly Gly Thr Gly Gly Thr Gly Thr Asp Ser Thr
259 35 40 45
261 Asp Pro Ser Gln Ala Ala Gln Ala Gly Gly Gln Gly Gly Val Gly Gly
262 50 55 60
265 Thr Gly Gly Ala Ala Gly Gln Gly Gly Thr Gly
266 65 70 75
269 <210> SEQ ID NO: 13
270 <211> LENGTH: 285
271 <212> TYPE: DNA
272 <213> ORGANISM: Mycobacterium marinum
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Mutant 67.1
277 <400> SEQUENCE: 13

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278 ggtcgaagac tatcggtatg ctccatagcg ttccgtcggg aagctgcatg ttgtcaaggg 60
 279 ttctgtcgac ctctcggcga cccatgaatc ccgatatgtg cgtgaagaaa ccgtacgaga 120
 280 tgctgatcac ctctgtggcg gtcgccttcg atatcgggat gcgcaccaat ccctcaatcc 180
 281 ggccggccac gttttccctt tccaccctgt cgacgagtggt gtgtccgtta tggcctaaat 240
 282 aatccatctt gctgcctctt tctgaaatcg aatttattac tatcg 285

285 <210> SEQ ID NO: 14

286 <211> LENGTH: 93

287 <212> TYPE: PRT

288 <213> ORGANISM: Mycobacterium marinum

290 <220> FEATURE:

291 <223> OTHER INFORMATION: Mutant 67.1

293 <400> SEQUENCE: 14

294 Ser Lys Thr Ile Gly Met Leu His Ser Val Pro Ser Gly Ser Cys Met
 295 1 5 10 15
 297 Leu Ser Arg Val Ser Ser Thr Ser Arg Arg Pro Met Asn Pro Asp Ser
 298 20 25 30
 300 Gly Val Lys Lys Pro Tyr Glu Met Leu Ile Thr Ser Trp Ala Val Ala
 301 35 40 45
 303 Phe Asp Ile Gly Met Arg Thr Asn Pro Ser Ile Arg Pro Ala Thr Phe
 304 50 55 60
 306 Ser Leu Ser Thr Leu Ser Thr Ser Gly Cys Pro Leu Trp Pro Lys Ser
 307 65 70 75 80
 309 Ile Leu Leu Pro Leu Ser Glu Ile Glu Phe Ile Thr Ile
 310 85 90

312 <210> SEQ ID NO: 15

313 <211> LENGTH: 90

314 <212> TYPE: PRT

315 <213> ORGANISM: Mycobacterium marinum

317 <220> FEATURE:

318 <223> OTHER INFORMATION: Mutant 67.1

320 <400> SEQUENCE: 15

321 Val Glu Asp Tyr Arg Tyr Ala Pro Arg Ser Val Gly Lys Leu His Val
 322 1 5 10 15
 324 Val Lys Gly Phe Val Asp Leu Ser Ala Thr His Glu Ser Arg Trp Arg
 325 20 25 30
 327 Glu Glu Thr Val Arg Asp Ala Asp His Leu Val Gly Gly Arg Leu Arg
 328 35 40 45
 330 Tyr Arg Asp Ala His Gln Ser Leu Asn Pro Ala Gly His Val Phe Pro
 331 50 55 60
 333 Phe His Pro Val Asp Glu Trp Val Ser Val Met Ala Ile Ile His Leu
 334 65 70 75 80
 336 Ala Ala Ser Phe Asn Arg Ile Tyr Tyr Tyr
 337 85 90

339 <210> SEQ ID NO: 16

340 <211> LENGTH: 92

341 <212> TYPE: PRT

342 <213> ORGANISM: Mycobacterium marinum

344 <220> FEATURE:

345 <223> OTHER INFORMATION: 67.1

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/088,356

DATE: 08/20/2002
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Input Set : A:\EP.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 25,27,29,31,33,35,37,39,41,43,45,47,49,51,53,55,57,59,61,63
Seq#:4; N Pos. 20
Seq#:5; Xaa Pos. 6
Seq#:6; N Pos. 37,299
Seq#:7; Xaa Pos. 97
Seq#:25; N Pos. 184
Seq#:26; Xaa Pos. 57
Seq#:27; N Pos. 5,6,13,23,36,41,43,49,63,68,76,89
Seq#:28; Xaa Pos. 8,12,17,19,21,29,31
Seq#:29; N Pos. 27,30,32,33,34,48
Seq#:30; Xaa Pos. 9,10,11
Seq#:31; N Pos. 4,17,21,24,29,34,45,54,72
Seq#:32; Xaa Pos. 1,5,7,8,11,15,18,24
Seq#:33; Xaa Pos. 1,6,7,8,10,15,18,24
Seq#:34; Xaa Pos. 2,6,7,8,10,12
Seq#:35; N Pos. 3,21,30,41,46,51,54,58,71
Seq#:36; Xaa Pos. 10,14,16,18,20,24
Seq#:37; Xaa Pos. 1,7,10,13,16,17,18,23
Seq#:38; Xaa Pos. 1,7,10,13,15,17,18,19
Seq#:44; N Pos. 169
Seq#:44; Xaa Pos. 57

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/088,356

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Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:3; N Pos. 25,27,29,31,33,35,37,39,41,43,45,47,49,51,53,55,57,59,61,63
Seq#:4; N Pos. 20
Seq#:5; Xaa Pos. 6
Seq#:6; N Pos. 37,299
Seq#:7; Xaa Pos. 97
Seq#:25; N Pos. 184
Seq#:26; Xaa Pos. 57
Seq#:27; N Pos. 5,6,13,23,36,41,43,49,63,68,76,89
Seq#:28; Xaa Pos. 8,12,17,19,21,29,31
Seq#:29; N Pos. 27,30,32,33,34,48
Seq#:30; Xaa Pos. 9,10,11
Seq#:31; N Pos. 4,17,21,24,29,34,45,54,72
Seq#:32; Xaa Pos. 1,5,7,8,11,15,18,24
Seq#:33; Xaa Pos. 1,6,7,8,10,15,18,24
Seq#:34; Xaa Pos. 2,6,7,8,10,12
Seq#:35; N Pos. 3,21,30,41,46,51,54,58,71
Seq#:36; Xaa Pos. 10,14,16,18,20,24
Seq#:37; Xaa Pos. 1,7,10,13,16,17,18,23
Seq#:38; Xaa Pos. 1,7,10,13,15,17,18,19
Seq#:44; N Pos. 169
Seq#:44; Xaa Pos. 57

VERIFICATION SUMMARY
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Input Set : A:\EP.txt
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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:53 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:53 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:54 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:54 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:60
L:69 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:69 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:86 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:86 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:111 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:111 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:115 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:115 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:240
L:151 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:151 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:96
L:549 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:549 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:180
L:576 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:576 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:48
L:604 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:604 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:605 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:605 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:60
L:621 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:621 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:624 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:624 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:16
L:640 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:640 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:656 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:656 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:675 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31

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L:675 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:676 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:676 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:60
L:691 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:691 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
L:691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:694 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:694 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
L:694 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:16
L:709 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:709 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:712 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:712 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:16
L:727 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:727 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:745 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:745 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:745 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:746 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:746 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:60
L:761 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
L:761 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
L:761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:16
L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16
L:797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:16
L:937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:144
L:938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:192